

HGS

Human Genome Sciences, Inc.
Project Worksheet
tumor necrosis factor (TNF-alpha)

Fri, Dec 3, 1999
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Project Information

Project Name: tumor necrosis factor (TNF-alpha)
Project Code:
Project Status: Active
HGS Code: 25750
Clone ID: HTPAN08
Library: Human Pancreas Tumor
Patent Status:
PTO Serial #:
Created By: Ann Kim
Date Created: 2/8/94
Date Modified: 2/8/94

General Comments

HGS FULL LENGTH PROJECTS

HGS #: DATE:

CLONE DESIGNATION:

TISSUE SOURCE:

SB PROJECT #(if any):

GENE MATCH:

HGS SCIENTIST(S):

POTENTIAL MEDICAL APPLICATION:

BASIC RESEARCH APPLICATION:

POTENTIAL PHARMACEUTICAL COLLABORATORS:

POTENTIAL ACADEMIC COLLABORATORS:

PATENT INFORMATION:

RESULTS (Dated)

NUCLEOTIDE BLAST ANALYSIS:

PROTEIN BLAST ANALYSIS:

Query= HTPAN08R
(568 letters)

Translating both strands of query sequence in all 6 reading frames



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Project Information

Project Name	tumor necrosis factor (TNF-alpha)
Project Code	
Project Status	Active
HGS Code	25750
Clone ID	HTPAN08
Library	Human Pancreas Tumor
Patent Status	
PTO Serial #	
Created By	Ann Kim
Date Created	2/8/94
Date Modified	2/8/94

General Comments

HGS FULL LENGTH PROJECTS

HGS #: DATE:

CLONE DESIGNATION:

TISSUE SOURCE:

SB PROJECT #(if any):

GENE MATCH:

HGS SCIENTIST(S):

POTENTIAL MEDICAL APPLICATION:

BASIC RESEARCH APPLICATION:

POTENTIAL PHARMACEUTICAL COLLABORATORS:

POTENTIAL ACADEMIC COLLABORATORS:

PATENT INFORMATION:

RESULTS (Dated)

NUCLEOTIDE BLAST ANALYSIS:

PROTEIN BLAST ANALYSIS:

Query= HTPAN08R
(568 letters)

Translating both strands of query sequence in all 6 reading frames

Ruben EXHIBIT 2098
Ruben v. Wiley et al.
Interference No. 105,077
RX 2098



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Database: nr

107,605 sequences; 30,094,510 total letters.

Searching.....done

Sequences producing High-scoring Segment Pairs:	Reading Frame	High Score	Smallest Poisson Probability	
			P(N)	N
gp U03470 RNU03470_1	ligand for Fas antigen [Rattus n...	+1	84	0.00093
gp X01394 HSTINFR_3	Human mRNA for tumor necrosis fa...	+1	74	0.021
gp M30964 SYNHNMINF_1	Synthetic human tumor necrosis f...	+1	74	0.021
gp L09754 MUSCD30_1	CD30 antigen [Mus musculus]	+1	52	0.024
gp X02910 HSTINFA_1	TNF-alpha [Homo sapiens] >gp Z15...	+1	74	0.025
gp M10988 HUMINFAA_1	TNFA gene product [Homo sapiens]	+1	74	0.025
gp X62141 PSPTINF_1	tumor necrosis factor [Papio sp....	+1	74	0.025
gp M35592 SYNTNFTRP_1	Synthetic human tumor necrosis f...	+1	74	0.025
gp M29079 PIGINFA_1	Porcine tumor necrosis factor al...	+1	72	0.045
gp L19123 RATTINFA_1	tumor necrosis factor-alpha [Rat...	+1	72	0.048

WARNING: Descriptions of 71 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|U03470|RNU03470_1 ligand for Fas antigen [Rattus norvegicus]
Length = 278

Plus Strand HSPs:

Score = 84 (39.4 bits), Expect = 0.00093, P = 0.00093

Identities = 15/34 (44%), Positives = 23/34 (67%), Frame = +1

Query: 226 GHSFLSNLHLRNGELVIHEKGFYIYSQTYFRFQ 327
G + +S + + G LVI+E G Y++YS+ YFR Q

Sbjct: 164 GTALISCVKYKKCGGLVINEAGLYFVYSKVYFRGQ 197

Score = 53 (24.9 bits), Expect = 0.0021, Poisson P(2) = 0.0021

Identities = 10/29 (34%), Positives = 17/29 (58%), Frame = +1

Query: 394 YPGPILLMKSARIWVGLKMQIWXYSTIKG 480
YPG ++LM+ ++ QIW +S+ G

Sbjct: 215 YPGDLVLMEEKKLNYCTTGQIWAHSSYLG 243

>gp|X01394|HSTINFR_3 Human mRNA for tumor necrosis factor [Homo sapiens]
Length = 157

Plus Strand HSPs:



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Score = 74 (34.7 bits), Expect = 0.021, P = 0.021
Identities = 14/40 (35%), Positives = 23/40 (57%), Frame = +1

Query: 208 WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQ 327
W + R+ + + LR+ +LV+ +G Y IYSQ F+ Q
Sbjct: 28 WLNRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQ 67

>gp|M30964|SYNHUMTNF_1 Synthetic human tumor necrosis factor (TNF) gene,
complete cds. [Artificial gene] >gp|A00362|A00362_1 tumor necrosis
factor alpha [None]
Length = 158

Plus Strand HSPs:

Score = 74 (34.7 bits), Expect = 0.022, P = 0.021
Identities = 14/40 (35%), Positives = 23/40 (57%), Frame = +1

Query: 208 WESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQ 327
W + R+ + + LR+ +LV+ +G Y IYSQ F+ Q
Sbjct: 29 WLNRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQ 68

SECOND WALK PROTEIN BLAST:

Query= HTPAN08Rp01
(342 letters)

Translating both strands of query sequence in all 6 reading frames

Database: nr
107,605 sequences; 30,094,510 total letters.
Searching.....done

Sequences producing High-scoring Segment Pairs:	Reading	High Frame	Smallest Poisson Probability	
			P(N)	N
gp L11015 HUMLYTOXBA_1 lymphotoxin-beta [Homo sapiens]...	+1	78	0.0019	1
gp x64387 VCHAG_2 haemagglutinin associated prote...	+1	46	0.022	2
pir S25359 S25359 hypothetical protein YKL525 - y...	+1	42	0.20	3
gp x64097 VCRVC_7 V. cholerae DNA for RVC repeated...	+2	44	0.60	2
pir S15111 S15111 Hemorrhagic factor LHFII - Bush...	+1	38	0.76	2
gp x56015 MICOONNR_2 NADH dehydrogenase subunit 4 [M...	-1	40	0.77	2
gp M69077 PRDCG_13 Bacteriophage PRD1, complete ge...	-1	39	0.77	2
gp M33581 MUSMDR1A_1 Mouse P-glycoprotein (mdrla) mR...	+1	40	0.78	3
gp M30697 MUSMDRAA_1 Mouse multidrug resistance prot...	+1	40	0.78	3
gp X14828 CHINFA_1 Goat mRNA for tumour necrosis f...	+1	58	0.85	1
pir S06192 S06192 tumor necrosis factor alpha pre...	+1	58	0.85	1



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gp M22647 PIGAPOB02_1	Pig apolipoprotein B gene (Lpb) ... +2	36	0.89	3
gp X03614 PAMFHNL_1	Sendai virus (strain Z) genome ... -1	55	0.91	1
gp L19357 CRULGPB_1	lysosomal membrane glycoprotein... -2	54	0.92	1
gp M97501 HUMCLIP_1	cytoplasmic linker protein-170 ... +1	41	0.93	2
gp X64838 HSRESTIN_1	restin [Homo sapiens] >pir S226... +1	41	0.94	2
pir S13421 S13421	Globin - Brine shrimp 0.0 0.0... -1	36	0.95	3
pir JT0382 JT0382	apolipoprotein B - pig (fragmen... +2	36	0.95	3
gp M35105 RATCROS1B_1	Rat lung-derived L01 c-ros-1 pr... +1	38	0.96	3
gp X58886 SVLARGEPEP_2	reverse peptide [Sendai virus]	-1	54	0.97

WARNING: Descriptions of 2 database sequences were not reported due to the limiting value of parameter V = 20.

>gp|L11015|HUMLYTOXBA_1 lymphotoxin-beta [Homo sapiens] >gp|L11016|HUMLYTOXBB_1 lymphotoxin-beta [Homo sapiens] >pir|A46066|A46066 lymphotoxin beta - human | 0.0 0.0 0.0 0.0 0.0 0.0
Length = 244

Plus Strand HSPs:

Score = 78 (37.6 bits), Expect = 0.0019, P = 0.0019
Identities = 12/37 (32%), Positives = 25/37 (67%), Frame = +1

Query: 151 GGIXELKENDRILVSVINEHLIIDMDHEASFFGAFLVG 261
GG+ +L+ +R+ V+ + +D +FFGA +VG
Sbjct: 208 GGLVQLRRGERVYVNISHPDMDVFARGKTFFGAVMVG 244

LENGTH OF CLONE(nucleotides):

PREDICTED LENGTH OF FULL LENGTH:

METHOD TO OBTAIN FULL LENGTH:

TISSUE DISTRIBUTION (alternate splicing?):

PROTEIN EXPRESSION:

FUNCTIONAL STUDIES (completed and planned):

TERMINATION (REASON):

Protein BLAST Analysis

Protein BLAST of the Reverse sequence

Smallest



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Sequences producing High-scoring Segment Pairs:				Reading Frame	High Score	Poisson Probability P(N)	Poisson Probability N
gp U03470 RNU03470_1	ligand for Fas antigen [Rattus n...	+2	85	0.00028	1		
gp S52010 S52010_2	orf1 5' of EpoR, orf2 5' of EpoR...	-3	45	0.18	2		
gp X01394 HSTINFR_3	Human mRNA for tumor necrosis fa...	+2	65	0.21	1		
gp M30964 SYNHUMINF_1	Synthetic human tumor necrosis f...	+2	65	0.21	1		
gp X02910 HSTINFA_1	TNF-alpha [Homo sapiens] >gp Z15...	+2	65	0.23	1		
gp M10988 HUMINFAA_1	TNFA gene product [Homo sapiens]...	+2	65	0.23	1		
gp X62141 PSPTNF_1	tumor necrosis factor [Papio sp....	+2	65	0.23	1		
gp M35592 SYNINFTRP_1	Synthetic human tumor necrosis f...	+2	65	0.23	1		
pir C21124 C21124	Bkm-like sex-determining region ...	-1	39	0.49	2		
gp K01664 DRORSXA_1	D.melanogaster Bkm-like DNA (pro...	-1	39	0.49	2		

WARNING: Descriptions of 28 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|U03470|RNU03470_1 ligand for Fas antigen [Rattus norvegicus]
Length = 278

Plus Strand HSPs:

Score = 85 (39.4 bits), Expect = 0.00028, P = 0.00028
Identities = 15/34 (44%), Positives = 22/34 (64%), Frame = +2

Query: 86 GNXFLSNLHLRNGELVIHEKGYYIYSQTYFRFQ 187

G +S + + G LVI+E G Y++YS+ YFR Q

Objct: 164 GTALISGVKYKKQGLVINEAGLYFVYSKVYFRGQ 197

Protein BLAST of the CONTIG containing reverse sequence and second and third walks

Sequences producing High-scoring Segment Pairs:				Frame	Score	P(N)	N
gp U03470 RNU03470_1	ligand for Fas antigen [Rattus n...	+2	84	0.00029	1		
gp X01394 HSTINFR_3	Human mRNA for tumor necrosis fa...	+2	74	0.0085	1		
gp M30964 SYNHUMINF_1	Synthetic human tumor necrosis f...	+2	74	0.0086	1		
gp X02910 HSTINFA_1	TNF-alpha [Homo sapiens] >gp Z15...	+2	74	0.0098	1		
gp M10988 HUMINFAA_1	TNFA gene product [Homo sapiens]...	+2	74	0.0098	1		
gp X62141 PSPTNF_1	tumor necrosis factor [Papio sp....	+2	74	0.0098	1		
gp M35592 SYNINFTRP_1	Synthetic human tumor necrosis f...	+2	74	0.0098	1		
gp M35027 VACCG_237	Vaccinia virus, complete genome....	-2	46	0.011	2		
gp M29079 PIGINFA_1	Porcine tumor necrosis factor al...	+2	72	0.019	1		
gp L19123 RATTINFA_1	tumor necrosis factor-alpha [Rat...	+2	72	0.020	1		



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WARNING: Descriptions of 94 database sequences were not reported due to the limiting value of parameter V = 10.

>gp|U03470|RNU03470_1 ligand for Fas antigen [Rattus norvegicus]
Length = 278

Plus Strand HSPs:

Score = 84 (42.3 bits), Expect = 0.00029, P = 0.00029
Identities = 15/34 (44%), Positives = 23/34 (67%), Frame = +2

Query: 179 GHSFLSNLHLRNGLELVIHEKGFYIYSQTYFRFQ 280

 G + +S + + G LVI+E G Y++YS+ YFR Q

Sbjct: 164 GTALISGVKYKKGLVINEAGLYFVYSKVYFRGQ 197

>gp|X01394|HSTINFR_3 Human mRNA for tumor necrosis factor [Homo sapiens]
Length = 157

Plus Strand HSPs:

Score = 74 (37.3 bits), Expect = 0.0086, P = 0.0085
Identities = 14/40 (35%), Positives = 23/40 (57%), Frame = +2

Query: 161 WESSRSGHSFLSNLHLRNGLELVIHEKGFYIYSQTYFRFQ 280

 W + R+ + + LR+ +LV+ +G Y IYSQ F+ Q

Sbjct: 28 WLNRANALLANGVELRDNQLVVPSEGGLYLIYSQVLFKGQ 67

>gp|M30964|SYNHUMINF_1 Synthetic human tumor necrosis factor (TNF) gene,
complete cds. [Artificial gene] >gp|A00362|A00362_1 tumor necrosis
factor alpha [None]
Length = 158

Plus Strand HSPs:

Score = 74 (37.3 bits), Expect = 0.0086, P = 0.0086
Identities = 14/40 (35%), Positives = 23/40 (57%), Frame = +2

Query: 161 WESSRSGHSFLSNLHLRNGLELVIHEKGFYIYSQTYFRFQ 280

 W + R+ + + LR+ +LV+ +G Y IYSQ F+ Q

Sbjct: 29 WLNRANALLANGVELRDNQLVVPSEGGLYLIYSQVLFKGQ 68

Query= HTPAN08Rev + Walks+ Forward Sequences
(1198 letters)



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Translating both strands of query sequence in all 6 reading frames

Database: nr
113,553 sequences; 31,868,292 total letters.
Searching.....done

Sequences producing High-scoring Segment Pairs:		Reading Frame	High Score	Smallest Poisson Probability	
				P(N)	N
pir S A40201	artifact-warning sequence (trans... +1	241	2.7e-77	3	
pir S C40201	artifact-warning sequence (trans... +3	246	1.3e-59	2	
pir S F40201	artifact-warning sequence (trans... +1	180	1.0e-21	2	
pir S D40201	artifact-warning sequence (trans... +1	81	2.1e-19	4	
gp X55777 HSMHCHHS_2	H.sapiens Mahlavi hepatocellular... +1	190	2.3e-19	1	
gp L27065 HUMNF2A_1	NF2 gene product [Homo sapiens] -3	139	3.7e-14	1	
pir S E40201	artifact-warning sequence (trans... +3	98	2.5e-12	4	
gp L20321 HUMSTK2A_1	protein serine/threonine kinase ... -1	137	3.7e-12	1	
gp S58722 S58722_1	X-linked retinopathy protein {3'... -1	128	1.8e-11	1	
pir S A46010	X-linked retinopathy protein (C... -1	128	1.8e-11	1	
gp M84237 HUMIGTB1A_2	integrin beta-1 subunit [Homo sa... -3	116	9.6e-11	1	
pir S A42442	beta 1 integrin subunit, beta 1S... -3	116	9.6e-11	1	
gp L24521 HUMIRRP_1	transformation-related protein [... -3	120	9.7e-10	1	
gp L11672 HUMKRUPZN_1	zinc finger protein [Homo sapiens] +2	108	6.1e-08	1	
gp U03470 RNU03470_1	ligand for Fas antigen [Rattus n... +1	84	1.3e-06	2	
gp X14828 CHINFA_1	Goat mRNA for tumour necrosis fa... +1	65	2.8e-06	2	
pir S S06192	tumor necrosis factor alpha prec... +1	65	2.8e-06	2	
pir S B26359	decay-accelerating factor 2 prec... -3	96	5.3e-06	1	
gp L26953 HUMPROTXA_1	Homo sapiens chromosomal protein... +1	101	6.2e-06	1	
gp A06305 A06305_1	lymphotoxin [None] +1	99	7.2e-06	1	
gp X77317 CHINFAMR_1	tumour necrosis factor alpha [Ca... +1	63	7.8e-06	2	
pir S B32877	tumor necrosis factor beta precu... +1	99	8.3e-06	1	
pir S S34742	lymphotoxin - human +1	99	8.3e-06	1	
pir S S26951	tumor necrosis factor beta - human +1	99	8.3e-06	1	
gp A00324 A00324_1	tumor necrosis factor beta [Arti... +1	99	8.4e-06	1	

>gp|U03470|RNU03470_1 ligand for Fas antigen [Rattus norvegicus]
Length = 278

Plus Strand HSPs:

Score = 84 (40.3 bits), Expect = 0.0017, P = 0.0017
Identities = 15/34 (44%), Positives = 23/34 (67%), Frame = +1

Query: 85 GHSFLSNLHLRNGLELVIHEKGFYIYSQTYFRFQ 186

G + +S + + G LVI+E G Y++YS+ YFR Q

Sbjct: 164 GTALISGVKYKKGGLVINEAGLYFVYSKVYFRGQ 197



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Score = 66 (31.7 bits), Expect = 1.3e-06, Poisson P(2) = 1.3e-06
Identities = 12/39 (30%), Positives = 22/39 (56%), Frame = +1

Query: 325 YSTYQGGIFELKENDRILVSVINELIIDMDHEASFFGAF 441
+S Y G +F L D + V+++ LI+ + +FFG +
Sbjct: 238 HSSYLGAVFNLTVADELYVNISQLSLINFEESKTFGGLY 276

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